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TECH CENTER 1600/2900

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/489,198A

DATE: 09/20/2001

TIME: 12:57:07

Input Set : A:\06501-054001.txt

Output Set: N:\CRF3\09202001\I489198A.raw

PS

4 <110> APPLICANT: Kato, Shigeaki
5 Takeyama, Ken-Ichi
6 Kitanaka, Sachiko
8 <120> TITLE OF INVENTION: GENE SCREENING METHOD USING NUCLEAR
9 RECEPTOR
11 <130> FILE REFERENCE: 06501-054001
13 <140> CURRENT APPLICATION NUMBER: 09/489,198A
14 <141> CURRENT FILING DATE: 2000-01-20
16 <150> PRIOR APPLICATION NUMBER: PCT/JP98/03280
17 <151> PRIOR FILING DATE: 1998-07-22
19 <150> PRIOR APPLICATION NUMBER: JP 9/212624
20 <151> PRIOR FILING DATE: 1997-07-22
22 <160> NUMBER OF SEQ ID NOS: 4
24 <170> SOFTWARE: FastSEQ for Windows Version 4.0
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 507
28 <212> TYPE: PRT
29 <213> ORGANISM: Mus musculus
31 <400> SEQUENCE: 1
32 Met Thr Gln Ala Val Lys Leu Ala Ser Arg Val Phe His Arg Ile His
33 1 5 10 15
34 Leu Pro Leu Gln Leu Asp Ala Ser Leu Gly Ser Arg Gly Ser Glu Ser
35 20 25 30
36 Val Leu Arg Ser Leu Ser Asp Ile Pro Gly Pro Ser Thr Leu Ser Phe
37 35 40 45
38 Leu Ala Glu Leu Phe Cys Lys Gly Gly Leu Ser Arg Leu His Glu Leu
39 50 55 60
40 Gln Val His Gly Ala Ala Arg Tyr Gly Pro Ile Trp Ser Gly Ser Phe
41 65 70 75 80
42 Gly Thr Leu Arg Thr Val Tyr Val Ala Asp Pro Thr Leu Val Glu Gln
43 85 90 95
44 Leu Leu Arg Gln Glu Ser His Cys Pro Glu Arg Cys Ser Phe Ser Ser
45 100 105 110
46 Trp Ala Glu His Arg Arg Arg His Gln Arg Ala Cys Gly Leu Leu Thr
47 115 120 125
48 Ala Asp Gly Glu Glu Trp Gln Arg Leu Arg Ser Leu Leu Ala Pro Leu
49 130 135 140
50 Leu Leu Arg Pro Gln Ala Ala Ala Gly Tyr Ala Gly Thr Leu Asp Asn
51 145 150 155 160
52 Val Val Arg Asp Leu Val Arg Arg Leu Arg Arg Gln Arg Gly Arg Gly
53 165 170 175
54 Ser Gly Leu Pro Gly Leu Val Leu Asp Val Ala Gly Glu Phe Tyr Lys
55 180 185 190
56 Phe Gly Leu Glu Ser Ile Gly Ala Val Leu Leu Gly Ser Arg Leu Gly
57 195 200 205
58 Cys Leu Glu Ala Glu Val Pro Pro Asp Thr Glu Thr Phe Ile His Ala
59 210 215 220

ENTERED

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60 Val Gly Ser Val Phe Val Ser Thr Leu Leu Thr Met Ala Met Pro Asn
61 225 230 235 240
62 Trp Leu His His Leu Ile Pro Gly Pro Trp Ala Arg Leu Cys Arg Asp
63 245 250 255
64 Trp Asp Gln Met Phe Ala Phe Ala Gln Arg His Val Glu Leu Arg Glu
65 260 265 270
66 Gly Glu Ala Ala Met Arg Asn Gln Gly Lys Pro Glu Glu Asp Met Pro
67 275 280 285
68 Ser Gly His His Leu Thr His Phe Leu Phe Arg Glu Lys Val Ser Val
69 290 295 300
70 Gln Ser Ile Val Gly Asn Val Thr Glu Leu Leu Ala Gly Val Asp
71 305 310 315 320
72 Thr Val Ser Asn Thr Leu Ser Trp Thr Leu Tyr Glu Leu Ser Arg His
73 325 330 335
74 Pro Asp Val Gln Thr Ala Leu His Ser Glu Ile Thr Ala Gly Thr Arg
75 340 345 350
76 Gly Ser Cys Ala His Pro His Gly Thr Ala Leu Ser Gln Leu Pro Leu
77 355 360 365
78 Leu Lys Ala Val Ile Lys Glu Val Leu Arg Leu Tyr Pro Val Val Pro
79 370 375 380
80 Gly Asn Ser Arg Val Pro Asp Arg Asp Ile Arg Val Gly Asn Tyr Val
81 385 390 395 400
82 Ile Pro Gln Asp Thr Leu Val Ser Leu Cys His Tyr Ala Thr Ser Arg
83 405 410 415
84 Asp Pro Thr Gln Phe Pro Asp Pro Asn Ser Phe Asn Pro Ala Arg Trp
85 420 425 430
86 Leu Gly Glu Gly Pro Thr Pro His Pro Phe Ala Ser Leu Pro Phe Gly
87 435 440 445
88 Phe Gly Lys Arg Ser Cys Ile Gly Arg Arg Leu Ala Glu Leu Glu Leu
89 450 455 460
90 Gln Met Ala Leu Ser Gln Ile Leu Thr His Phe Glu Val Leu Pro Glu
91 465 470 475 480
92 Pro Gly Ala Leu Pro Ile Lys Pro Met Thr Arg Thr Val Leu Val Pro
93 485 490 495
94 Glu Arg Ser Ile Asn Leu Gln Phe Val Asp Arg
95 500 505
97 <210> SEQ ID NO: 2
98 <211> LENGTH: 508
99 <212> TYPE: PRT
100 <213> ORGANISM: Homo sapiens
102 <400> SEQUENCE: 2
103 Met Thr Gln Thr Leu Lys Tyr Ala Ser Arg Val Phe His Arg Val Arg
104 1 5 10 15
105 Trp Ala Pro Glu Leu Gly Ala Ser Leu Gly Tyr Arg Glu Tyr His Ser
106 20 25 30
107 Ala Arg Arg Ser Leu Ala Asp Ile Pro Gly Pro Ser Thr Pro Ser Phe
108 35 40 45
109 Leu Ala Glu Leu Phe Cys Lys Gly Gly Leu Ser Arg Leu His Glu Leu
110 50 55 60

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111 Gln Val Gln Gly Ala Ala His Phe Gly Pro Val Trp Leu Ala Ser Phe
112 65 70 75 80
113 Gly Thr Val Arg Thr Val Tyr Val Ala Ala Pro Ala Leu Val Glu Glu
114 85 90 95
115 Leu Leu Arg Gln Glu Gly Pro Arg Pro Glu Arg Cys Ser Phe Ser Pro
116 100 105 110
117 Trp Thr Glu His Arg Arg Cys Arg Gln Arg Ala Cys Gly Leu Leu Thr
118 115 120 125
119 Ala Glu Gly Glu Glu Trp Gln Arg Leu Arg Ser Leu Leu Ala Pro Leu
120 130 135 140
121 Leu Leu Arg Pro Gln Ala Ala Arg Tyr Ala Gly Thr Leu Asn Asn
122 145 150 155 160
123 Val Val Cys Asp Leu Val Arg Arg Leu Arg Arg Gln Arg Gly Arg Gly
124 165 170 175
125 Thr Gly Pro Pro Ala Leu Val Arg Asp Val Ala Gly Glu Phe Tyr Lys
126 180 185 190
127 Phe Gly Leu Glu Gly Ile Ala Ala Val Leu Leu Gly Ser Arg Leu Gly
128 195 200 205
129 Cys Leu Glu Ala Gln Val Pro Pro Asp Thr Glu Thr Phe Ile Arg Ala
130 210 215 220
131 Val Gly Ser Val Phe Val Ser Thr Leu Leu Thr Met Ala Met Pro His
132 225 230 235 240
133 Trp Leu Arg His Leu Val Pro Gly Pro Trp Gly Arg Leu Cys Arg Asp
134 245 250 255
135 Trp Asp Gln Met Phe Ala Phe Ala Gln Arg His Val Glu Arg Arg Glu
136 260 265 270
137 Ala Glu Ala Ala Met Arg Asn Gly Gly Gln Pro Glu Lys Asp Leu Glu
138 275 280 285
139 Ser Gly Ala His Leu Thr His Phe Leu Phe Arg Glu Glu Leu Pro Ala
140 290 295 300
141 Gln Ser Ile Leu Gly Asn Val Thr Glu Leu Leu Ala Gly Val Asp
142 305 310 315 320
143 Thr Val Ser Asn Thr Leu Ser Trp Ala Leu Tyr Glu Leu Ser Arg His
144 325 330 335
145 Pro Glu Val Gln Thr Ala Leu His Ser Glu Ile Thr Ala Ala Leu Ser
146 340 345 350
147 Pro Gly Ser Ser Ala Tyr Pro Ser Ala Thr Val Leu Ser Gln Leu Pro
148 355 360 365
149 Leu Leu Lys Ala Val Val Lys Glu Val Leu Arg Leu Tyr Pro Val Val
150 370 375 380
151 Pro Gly Asn Ser Arg Val Pro Asp Lys Asp Ile His Val Gly Asp Tyr
152 385 390 395 400
153 Ile Ile Pro Lys Asn Thr Leu Val Thr Leu Cys His Tyr Ala Thr Ser
154 405 410 415
155 Arg Asp Pro Ala Gln Phe Pro Glu Pro Asn Ser Phe Arg Pro Ala Arg
156 420 425 430
157 Trp Leu Gly Glu Gly Pro Thr Pro His Pro Phe Ala Ser Leu Pro Phe
158 435 440 445
159 Gly Phe Gly Lys Arg Ser Cys Met Gly Arg Arg Leu Ala Glu Leu Glu

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Input Set : A:\06501-054001.txt
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160	450	455	460	
161	Leu Gln Met Ala Leu Ala Gln Ile Leu Thr His Phe Glu Val Gln Pro			
162	465	470	475	480
163	Glu Pro Gly Ala Ala Pro Val Arg Pro Lys Thr Arg Thr Val Leu Val			
164	485	490		495
165	Pro Glu Arg Ser Ile Asn Leu Gln Phe Leu Asp Arg			
166	500	505		
168	<210> SEQ ID NO: 3			
169	<211> LENGTH: 2386			
170	<212> TYPE: DNA			
171	<213> ORGANISM: Mus musculus			
173	<220> FEATURE:			
174	<221> NAME/KEY: CDS			
175	<222> LOCATION: (30)...(1550)			
177	<400> SEQUENCE: 3			
178	ctctcgaagc agactcccca aacacagac atg acc cag gca gtc aag ctc gcc			53
179	Met Thr Gln Ala Val Lys Leu Ala			
180	1	5		
182	tcc aga gtt ttt cac cga atc cac ctg cct ctg cag ctg gat gcc tcg			101
183	Ser Arg Val Phe His Arg Ile His Leu Pro Leu Gln Leu Asp Ala Ser			
184	10	15	20	
186	ctg ggc tcc aga ggc agt gag tcg gtt ctc cgg agc ttg tct gac atc			149
187	Leu Gly Ser Arg Gly Ser Glu Ser Val Leu Arg Ser Leu Ser Asp Ile			
188	25	30	35	40
190	cct ggg ccc tct aca ctc agc ttc ctg gct gaa ctc ttc tgc aaa ggg			197
191	Pro Gly Pro Ser Thr Leu Ser Phe Leu Ala Glu Leu Phe Cys Lys Gly			
192	45	50	55	
194	ggg ctg tcc agg ctg cat gaa ctg cag gtg cat ggc gct gcg cgg tac			245
195	Gly Leu Ser Arg Leu His Glu Leu Gln Val His Gly Ala Ala Arg Tyr			
196	60	65	70	
198	ggg cca ata tgg tct ggc agc ttt ggg aca ctt cgc aca gtt tac gtt			293
199	Gly Pro Ile Trp Ser Gly Ser Phe Gly Thr Leu Arg Thr Val Tyr Val			
200	75	80	85	
202	gcc gac cct aca ctt gtg gag cag ctc ctg cga caa gaa agt cac tgt			341
203	Ala Asp Pro Thr Leu Val Glu Gln Leu Leu Arg Gln Glu Ser His Cys			
204	90	95	100	
206	cca gag cgc tgt agt ttc tca tca tgg gca gag cac cgt cgc cgc cac			389
207	Pro Glu Arg Cys Ser Phe Ser Ser Trp Ala Glu His Arg Arg Arg His			
208	105	110	115	120
210	cag cgt gct tgc gga ttg cta acg gcg gat ggt gaa gaa tgg cag agg			437
211	Gln Arg Ala Cys Gly Leu Leu Thr Ala Asp Gly Glu Glu Trp Gln Arg			
212	125	130	135	
214	ctc cga agt ctt ctg gcc ccg ctc ctc cgg cca caa gca gcc gcg			485
215	Leu Arg Ser Leu Leu Ala Pro Leu Leu Arg Pro Gln Ala Ala Ala			
216	140	145	150	
218	ggc tat gct gga act ctg gac aac gtg gtc cgt gac ctt gtg cga cga			533
219	Gly Tyr Ala Gly Thr Leu Asp Asn Val Val Arg Asp Leu Val Arg Arg			
220	155	160	165	
222	cta agg cgc cag cgg gga cgt ggc tct ggg cta ccc ggc cta gtt ctg			581

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Input Set : A:\06501-054001.txt

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223	Leu	Arg	Arg	Gln	Arg	Gly	Arg	Gly	Ser	Gly	Leu	Pro	Gly	Leu	Val	Leu
224	170				175						180					
226	gac	gtg	gca	gga	gag	ttt	tac	aaa	ttt	ggc	cta	gaa	agt	ata	ggc	gcg
227	Asp	Val	Ala	Gly	Glu	Phe	Tyr	Lys	Phe	Gly	Leu	Glu	Ser	Ile	Gly	Ala
228	185				190					195				200		
230	gtg	ctg	ctg	gga	tcg	cgc	ctg	ggc	tgc	cta	gag	gct	gaa	gtc	cct	cct
231	Val	Leu	Leu	Gly	Ser	Arg	Leu	Gly	Cys	Leu	Glu	Ala	Glu	Val	Pro	Pro
232						205				210				215		
234	gac	aca	gaa	acc	tcc	ata	cat	gca	gtg	ggc	tca	gtg	ttt	gtg	tct	aca
235	Asp	Thr	Glu	Thr	Phe	Ile	His	Ala	Val	Gly	Ser	Val	Phe	Val	Ser	Thr
236						220				225				230		
238	ctc	ttg	acc	atg	gcf	atg	ccc	aac	tgg	tgg	cac	cac	ctt	ata	cct	gga
239	Leu	Leu	Thr	Met	Ala	Met	Pro	Asn	Trp	Leu	His	His	Leu	Ile	Pro	Gly
240						235				240				245		
242	ccc	tgg	gcc	cgc	ctc	tgc	cga	gac	tgg	gat	cag	atg	ttt	gcc	ttt	gcc
243	Pro	Trp	Ala	Arg	Leu	Cys	Arg	Asp	Trp	Asp	Gln	Met	Phe	Ala	Phe	Ala
244						250				255				260		
246	cag	agg	cac	gtg	gag	ctg	cga	gaa	ggt	gaa	gct	gcf	atg	agg	aac	cag
247	Gln	Arg	His	Val	Glu	Leu	Arg	Glu	Gly	Glu	Ala	Ala	Met	Arg	Asn	Gln
248						265				270				275		280
250	gga	aag	cct	gag	gag	gat	atg	ccg	tct	ggg	cat	cac	tta	acc	cac	ttc
251	Gly	Lys	Pro	Glu	Glu	Asp	Met	Pro	Ser	Gly	His	His	Leu	Thr	His	Phe
252						285				290				295		
254	ctt	ttt	cg	gaa	aag	gtg	tct	gtc	cag	tcc	ata	gtg	ggg	aat	gtg	aca
255	Leu	Phe	Arg	Glu	Lys	Val	Ser	Val	Gln	Ser	Ile	Val	Gly	Asn	Val	Thr
256						300				305				310		
258	gag	cta	cta	ctg	gct	gga	gtg	gac	acg	gta	tcc	aat	acg	ctc	tcc	tgg
259	Glu	Leu	Leu	Leu	Ala	Gly	Val	Asp	Thr	Val	Ser	Asn	Thr	Leu	Ser	Trp
260						315				320				325		
262	aca	ctc	tat	gag	ctt	tcc	cg	cac	ccc	gat	gtc	cag	act	gca	ctc	cac
263	Thr	Leu	Tyr	Glu	Leu	Ser	Arg	His	Pro	Asp	Val	Gln	Thr	Ala	Leu	His
264						330				335				340		
266	tct	gag	atc	aca	gct	ggg	acc	cgt	ggc	tcc	tgt	gcc	cac	ccc	cat	ggc
267	Ser	Glu	Ile	Thr	Ala	Gly	Thr	Arg	Gly	Ser	Cys	Ala	His	Pro	His	Gly
268						345				350				355		360
270	act	gct	ctg	cag	ctg	ccc	ctg	tta	aag	gct	gtg	atc	aaa	gaa	gtg	
271	Thr	Ala	Leu	Ser	Gln	Leu	Pro	Leu	Leu	Lys	Ala	Val	Ile	Lys	Glu	Val
272						365				370				375		
274	ttg	aga	ttg	tac	cct	gtg	gta	cct	ggg	aat	tcc	cgt	gtc	cca	gac	aga
275	Leu	Arg	Leu	Tyr	Pro	Val	Val	Pro	Gly	Asn	Ser	Arg	Val	Pro	Asp	Arg
276						380				385				390		
278	gac	atc	cgt	gta	gga	aac	tat	gta	att	ccc	caa	gat	acg	cta	gtc	tcc
279	Asp	Ile	Arg	Val	Gly	Asn	Tyr	Val	Ile	Pro	Gln	Asp	Thr	Leu	Val	Ser
280						395				400				405		
282	cta	tgt	cac	tat	gcc	act	tca	agg	gac	ccc	aca	cag	ttt	cca	gac	ccc
283	Leu	Cys	His	Tyr	Ala	Thr	Ser	Arg	Asp	Pro	Thr	Gln	Phe	Pro	Asp	Pro
284						410				415				420		
286	aac	tct	ttt	aat	cca	gct	cgc	tgg	ctg	ggg	gag	ggt	ccg	acc	ccc	cac
287	Asn	Ser	Phe	Asn	Pro	Ala	Arg	Trp	Leu	Gly	Glu	Gly	Pro	Thr	Pro	His

→ Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/489,198A

DATE: 09/20/2001
TIME: 12:57:08

Input Set : A:\06501-054001.txt
Output Set: N:\CRF3\09202001\I489198A.raw

L:473 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4